FIG. 1B

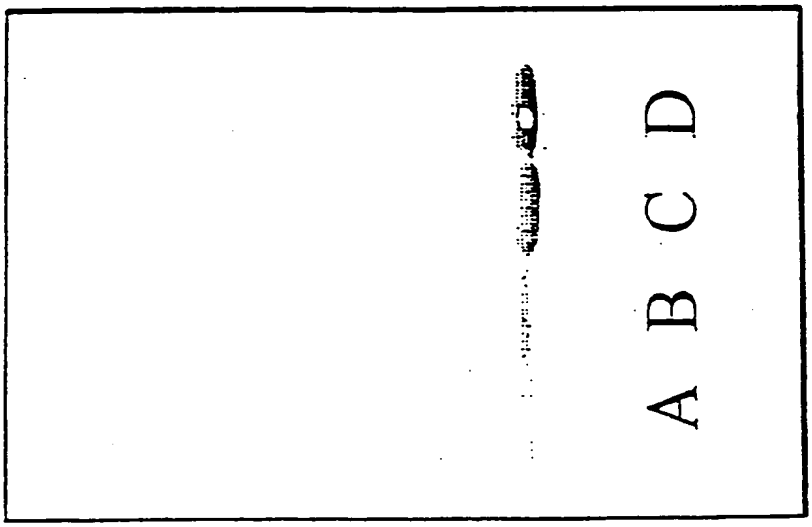

FIG. 1A

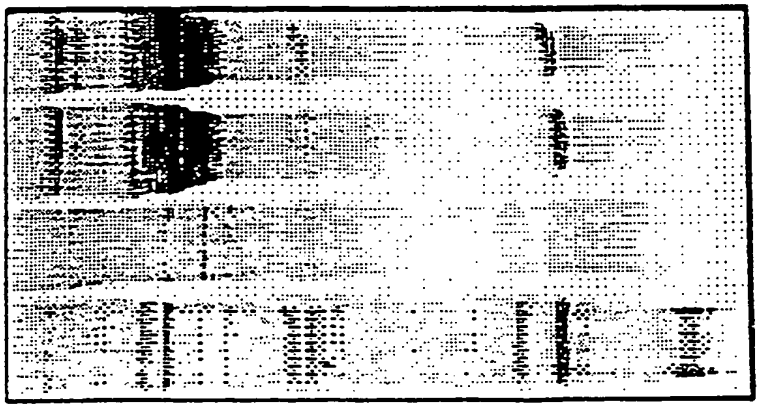

FIG. 2

```
1   AAACCAAGGCAGGACACAGCAGCCATGAAGGCCTTCGTTGCAGTCGCCCTTTTGTCTGCA   60
                          M  K  A  F  V  A  V  A  L  L  S  A

61  GTTTCCGTGGCACATGCTGCCCTCAAGACTGACGTAGCCAGTGGACCTGCCGGTTCTGGT  120
    V  S  V  A  H  A  A  L  K  T  D  V  A  S  G  P  A  G  S  G

121 GCACTAAGTCTAGGAGTTGGAGGCTTCCCGTCCGGTGCTTCGCTTGGCAGCCTTAGTGGC  180
    A  L  S  L  G  V  G  G  F  P  S  G  A  S  L  G  S  L  S  G

181 GTAACCCTCTCTGGTGCTGGCTCTTCCGTGTCTGGCCGCCCTGGATCCCCTGGATCGGCT  240
    V  T  L  S  G  A  G  S  S  V  S  G  R  P  G  S  P  G  S  A

241 GGTCCTAGCTCTGGACCCGCAGTGTCG  267
    G  P  S  S  G  P  A  V  S
```

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FIG. 3

```
1    CGGACGCACACTCCTGCAGGAAGGTCATCTAGTTCCGCCAACATGAAGCTGCTCTGTGCA   60
                                          M  K  L  L  C  A

61   CTAGCCCTCGTTGCCCTTGGACTTCCATTCGGCAGCGCTTACCTTGGTGGCTTCGGCGGC  120
     L  A  L  V  A  L  G  L  P  F  G  S  A  Y  L  G  G  F  G  G

121  CTCGGTGGTTGGGGTGGCGGTCTCGGTGCCATCTTTGGCCCAGGAGCTTATCCCGGTTTC  180
     L  G  G  W  G  G  G  L  G  A  I  F  G  P  G  A  Y  P  G  F

181  TATGGCCTTAACAGCGTGCACCTCTTGGGCGGCAGGTTCCACCATCTCTTCGGGCGATTC  240
     Y  G  L  N  S  V  H  L  L  G  G  R  F  H  H  L  F  G  R  F

241  CCGCCACCACCCGGTATTGGAGCTGCTGAAGCGCAGGGGAACCTAAGCCCATACCCTCTT  300
     P  P  P  P  G  I  G  A  A  E  A  Q  G  N  L  S  P  Y  P  L

301  GACATCAACACCGTCCAAGACCCGAACTGGCCACCCCATGGTACGCGTTGTCTACGGCGG  360
     D  I  N  T  V  Q  D  P  N  W  P  P  H  G  T  R  C  L  R  R

361  AGTCTTGCGGGAGCGCCTCTGACCCTGACCAGTCCCAATTCCACAGGATGTGCCTGTCCC  420
     S  L  A  G  A  P  L  T  L  T  S  P  N  S  T  G  C  A  C  P
```

```
421  AGTCCCCATTCCAGTGCCCCAGCCATACCCAGTCCCACACCCACGACAAGTTCCATACCC  480
     S  P  H  S  S  A  P  A  I  P  S  P  T  P  T  T  S  S  I  P

481  AGTGCCTAGTCCCTACCCCGTCCCAATCCACAGTAACACCGAAGTTCACAAGACCGACGT  540
     S  A

541  CGTCGCCGCTACTCCAGGAGGACCAGTCCTGCTCGGAGTCGGTGTCACCGGTGTCAGGCC  600

601  AGGCGAACCAAGGGTCGTGGCCTAAGCTTGATCCAATAGAAAGTCATAACAATTTAGTCA  660

661  GTGAGCTCCACGTAAATTATGCATTACAAATAAAGAAAAGTTTGTCTGGCAGTAAAAAAA  720

721  AAAAAAAAAA  730
```

FIG. 3(CONTD.)

FIG. 4

```
1   GATCGGCACGAGGTCAAGGGAGCCCTCCTTCAGCAACAACAAGCATCGCAGGTTAAGGGA   60
    D  R  H  E  V  K  G  A  L  L  Q  Q  Q  Q  A  S  Q  V  K  G

61  GCCCTCAAGGGAGCAATCAAGGGTGGTCTTCTTCAGCAACAAGCCCAATCCCAAGTCCAA  120
    A  L  K  G  A  I  K  G  G  L  L  Q  Q  Q  A  Q  S  Q  V  Q

121 GGAGCTCTTAAGGGAGCCGTCAAGGGAGCCCTCCTTCAGCAACAACAGGCATCACAGGTC  180
    G  A  L  K  G  A  V  K  G  A  L  L  Q  Q  Q  Q  A  S  Q  V

181 AAGGGAGCCCTCAAGGGAGCCATCAAGGTCTGTCTCCTTCATCAGCAAGCCCAATCCCAA  240
    K  G  A  L  K  G  A  I  K  V  C  L  L  H  Q  Q  A  Q  S  Q

241 TCCCAAGTTCAGGGAGCTCTTAAGGGAGCTG  271
    S  Q  V  Q  G  A  L  K  G  A
```


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FIG. 5

```
  1  GGAAGTAGCGAGCATCCGCACTGGGGTCTTTTTGGCTGCATTTGCTTTTCTTCTTTCAGC   60
      E  V  A  S  I  R  T  G  V  F  L  A  A  F  A  F  L  L  S  A

 61  GATCCATAACAATGGCCAGTCATGTGTAGATGCAGCCCCCACTCGACGTCCTATGCCATC  120
      I  H  N  N  G  Q  S  C  V  D  A  A  P  T  R  R  P  M  P  S

121  TCCTCCTGGATGTGCTGGTCCTGGCTGTTTTACTGGTATTGCTACTCTTCTAAGACCTGG  180
      P  P  G  C  A  G  P  G  C  F  T  G  I  A  T  L  L  R  P  G

181  TCAAGGACAGCAACCTGGTCAAGGACAGCAACCTGGTCAAGGGCGTCCTCCAATGCCACG  240
      Q  G  Q  Q  P  G  Q  G  Q  Q  P  G  Q  G  R  P  P  M  P  R

241  TCCAGGACCTGTTCCAGGAACATCTGGATCACCTCAAGGAAGACCCAATGGAGCACCTCG  300
      P  G  P  V  P  G  T  S  G  S  P  Q  G  R  P  N  G  A  P  R

301  TCCAGGACCTGTTCCTGGAACATCTGGATCACCTCAAGGAAGACCTAACGCAAGACCTCG  360
      P  G  P  V  P  G  T  S  G  S  P  Q  G  R  P  N  A  R  P  R

361  TCCAGGACCTGTTCCTGGAACACCAACTGTATCCTCTCCCGGATCATCTCCTGGGTCATC  420
      P  G  P  V  P  G  T  P  T  V  S  S  P  G  S  S  P  G  S  S
```

```
421  TCCAGGAATATCTCTAGGAACGCCTCTAGGAACACCTCTAGGAACACCTCAAGGATCACC  480
       P   G   I   S   L   G   T   P   L   G   T   P   L   G   T   P   Q   G   S   P

481  TTTTGGATCATCTCTTGGATCATCGATAGGATCACCTCCTGCAACATCTCCTGGATCATC  540
       F   G   S   S   L   G   S   S   I   G   S   P   P   A   T   S   P   G   S   S

541  TTCTCCGTCACCTCCTGGATCAGCGAATGTGAACCTGCTGGGTCCTCGACCAATTCGCGG  600
       S   P   S   P   P   G   S   A   N   V   N   L   L   G   P   R   P   I   R   G

601  TCCTGGAAGGCATTGACGGGACCAGTTCTGCTGTGTATTCCTCCGTGCACAATGAGGGAA  660
       P   G   R   H

661  GGCATTGATGGGACCAGTTCTGCTGTGTATTTCTCCGTGCACAGTGAGGGAATCTATCAA  720

721  TAGTGCAATAA  731
```

FIG. 5(CONTD.)

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```
1   GGCTTCGGCAGCCCACTCAGCGGTTTCGGCAGCCCACTCAGCGGTTTCGGCAGCCCACTC   60
    G  F  G  S  P  L  S  G  F  G  S  P  L  S  G  F  G  S  P  L

61  AGCGGCTTCGGCAGCCCACTCAGCGGATTCGGTAGCCCACTCAGCGGATTCGGTAGCCCA  120
    S  G  F  G  S  P  L  S  G  F  G  S  P  L  S  G  F  G  S  P

121 CTCAGCGGATTCGGTAGCCCATTCGGCAGCTACGGTCCCCTGTCCATGGGTCTCGGAGCC  180
    L  S  G  F  G  S  P  F  G  S  Y  G  P  L  S  M  G  L  G  A

181 CCCAGGAGATTCCCCGGCGACCTCCGCCTCATCTCTGAGCCCACCTCCCGCCTTCCCGTT  240
    P  R  R  F  P  G  D  L  R  L  I  S  E  P  T  S  R  L  P  V

241 AGCGATGCCGTCTACACCGCTGTCGTCCAGCCCGTCACAAGCGCAGTGGTCCACACCGAG  300
    S  D  A  V  Y  T  A  V  V  Q  P  V  T  S  A  V  V  H  T  E

301 GGTCCCCATGTCACCGGCCAAGTACAGGAACACGTTGCAATCTAAGCTTTTCTAACCGCA  360
    G  P  H  V  T  G  Q  V  Q  E  H  V  A  I

361 AGCTATATTACGACGGATTAGTCAACACAGTCATCTTAAGCAAATGTATCTAAAATAAAA  420

421 TTTATCTGCCT  431
```

FIG. 6

FIG. 7

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```
361  TTTTGGCTCTGCATACGGCGGCTACCCCGGCTACTATGGCTACTACTATCCCAGTGGCTA  420
       F   G   S   A   Y   G   G   Y   P   G   Y   Y   G   Y   Y   Y   P   S   G   Y

421  CGGTGGGGGCTACGGTGGTAGCTACGGTGGCAGCTACGGTGGTAGCTACACCTATCCCAA  480
     G   G   G   G   Y   G   G   S   Y   G   G   S   Y   G   G   S   Y   T   Y   P   N

481  CGTTCGGGCTTCAGCTGGTGCCGCAGCTTGAGCTTCTCCTTCAGCGTCACAGTAAGAAAT  540
       V   R   A   S   A   G   A   A   A   *

541  CATGGAGCACCCGATCGAGAAATACAGAGGTTCTCAAAAGCGTACGGGATGCCAACCAGC  600

601  AAGAAATTGCGCCGCAAAATGTTGAGAACAAATACAAGTTTTCTGTAAAAAAAAAA      656
```

FIG. 7(CONTD.)

FIG. 8

```
  1  ACGGACTAGGTTTCGCTGGCGTCCCTCTTATTGGCGGATACGGCTACGGTCCTTTCGTAG   60
       G  L  G  F  A  G  V  P  L  I  G  G  Y  G  Y  G  P  F  V  G

 61  GAGCCTTCGCGTACGGCTTGTGGGGTGGCCTCGGTGGCTATGGCTACCCTGCCTTCGGAC  120
       A  F  A  Y  G  L  W  G  G  L  G  G  Y  G  Y  P  A  F  G  L

121  TCTCCTGGGTTCCACATGGTTTTGGAGGCTTTGGAGCTTCTCCGTCTGCTGCTGGTTTCC  180
       S  W  V  P  H  G  F  G  G  F  G  A  S  P  S  A  A  G  F  R

181  GCTCGCTTTGGAGCCTCTT  199
       S  L  W  S  L
```

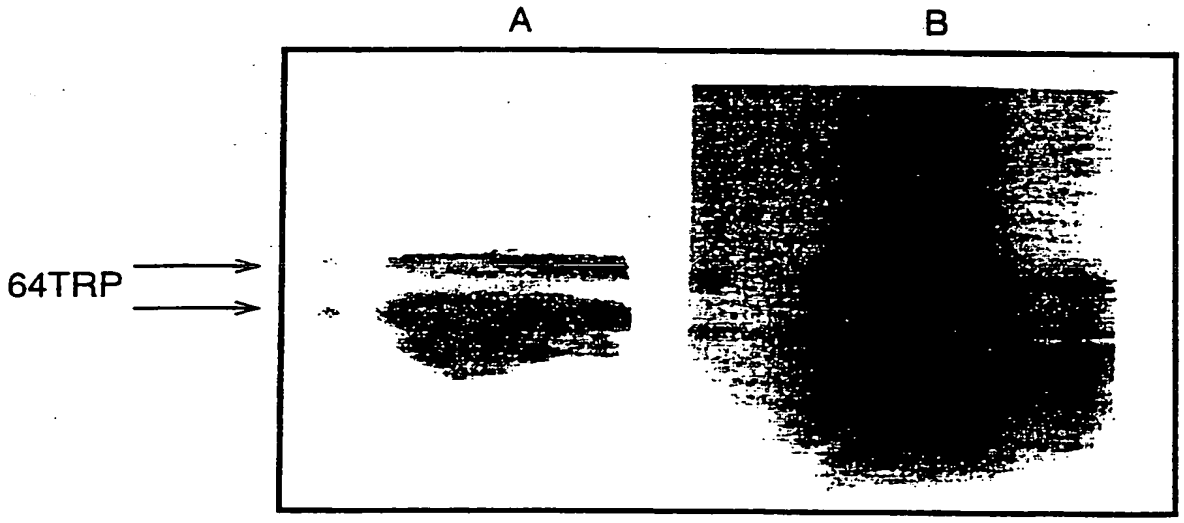
FIG. 9

```
R.appendiculatus
      GLGFAGVPLIGGYGYGPFVGAFAYGLWGGLGGYGYPAFGLSWVPHGFGGFGASP
      |.|: |.. :||||||: :|:::||  : :|||||.| :   | :::||:||::
      GYGY.GAKKVGGYGYGAKLGGYGYG..AKIGGYGYGAKSGIQV.RALGGYGAGA

P.californica
```

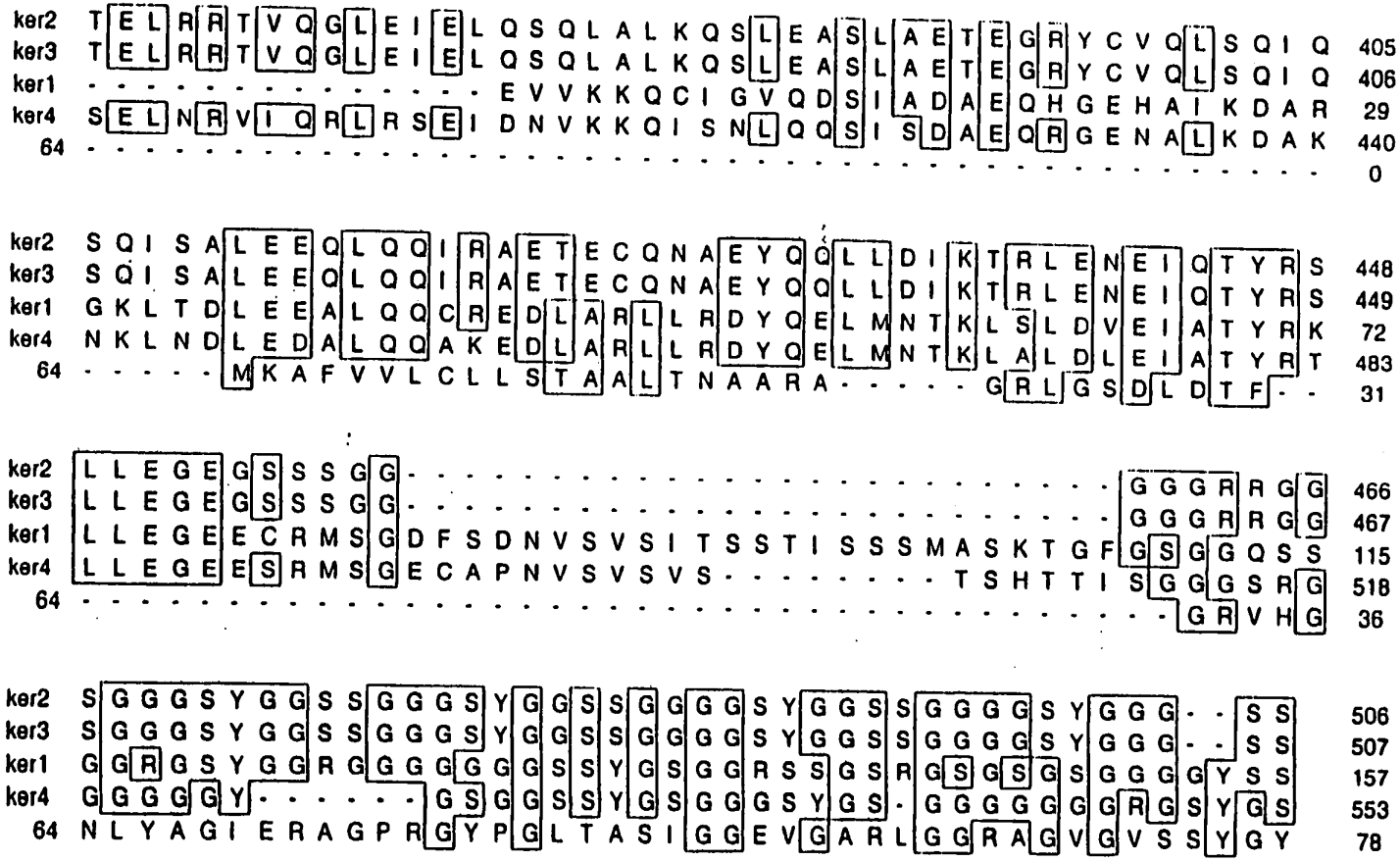
FIG. 10

EXPRESSION OF RECOMBINANT (TRUNCATED) STRUCTURAL PROTEIN, 64TRP IN *Escherichia coli* CELLS



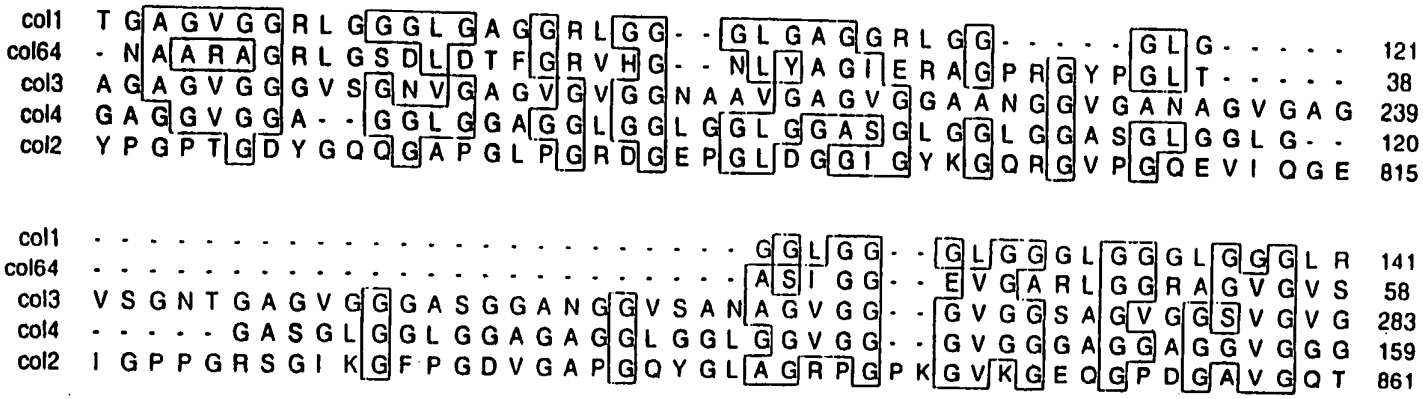
SDS-PAGE: (A) AND (B) WESTERN BLOT (USING ANTI-64TRP ANTISERUM) AND COOMASSIE BLUE STAINED 15% POLYACRYLAMIDE GEL, RESPECTIVELY OF IPTG-INDUCED *E.coli* CELLS EXPRESSING 64TRP PROTEIN. SAMPLES WERE SOLUBULISED AT 100^{o} C IN SDS PRIOR TO LOADING THE GELS.

FIG. 11a cDNA inferred sequence alignment between the protein sequence of 64P and other related structural proteins.



Sequences are: ker1=keratin complex2 basic protein, ker2=mouse keratin, ker3=mouse epidermalK protein, ker4=human keratin protein, 64P=*R. appendiculatus* putative structural protein

FIG. 11b cDNA inferred sequence alignment between the protein sequences of 64TRP and other structural proteins.



Sequences are: col1=Glycine-rich GX protein-motif LGG, col2=collagen type Iv alpha protein, col3=IPIB2 precursor protein, col4=Glycine rich cell wall protein, 64TRP=*R. appendiculatus* truncated structural protein

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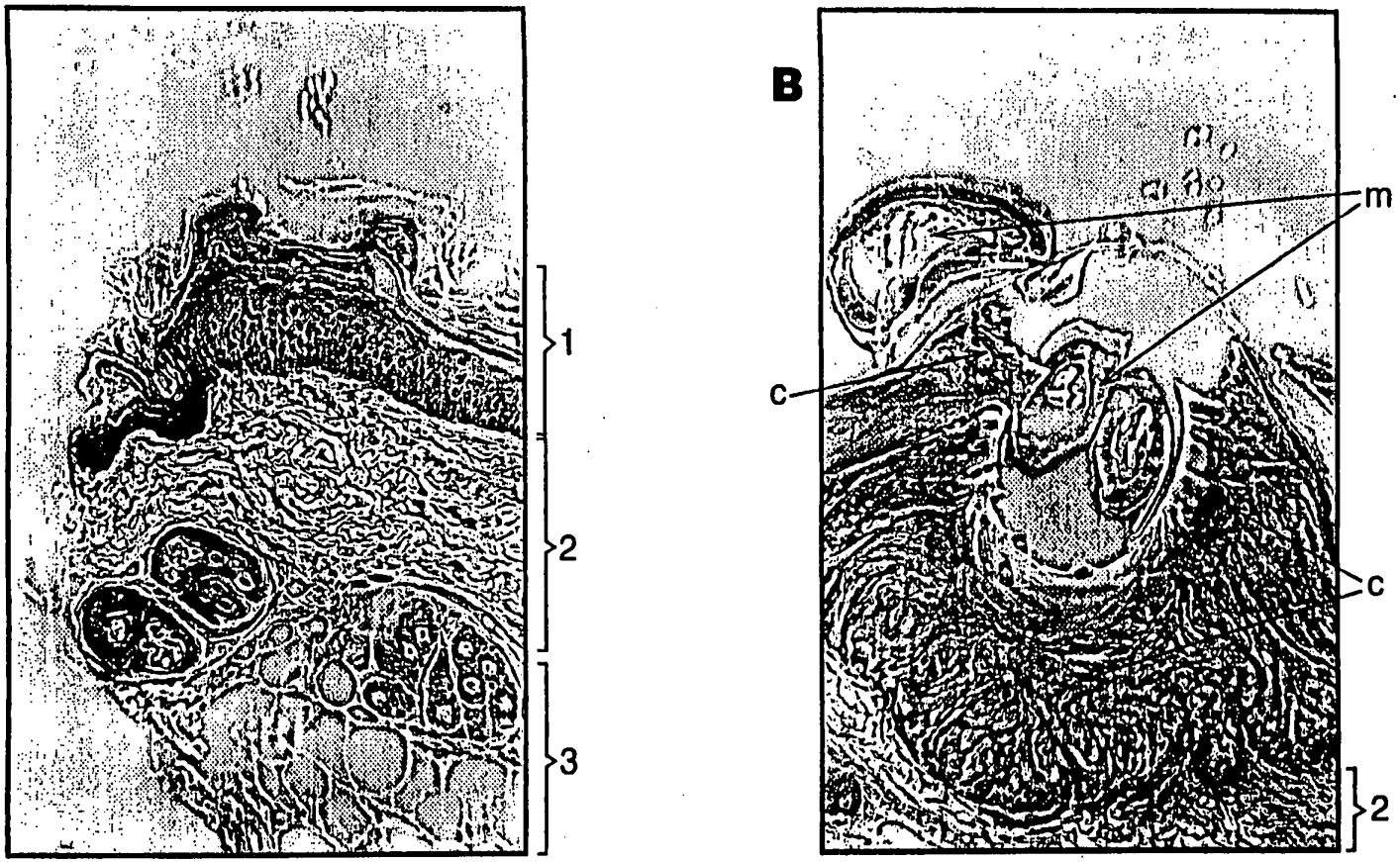
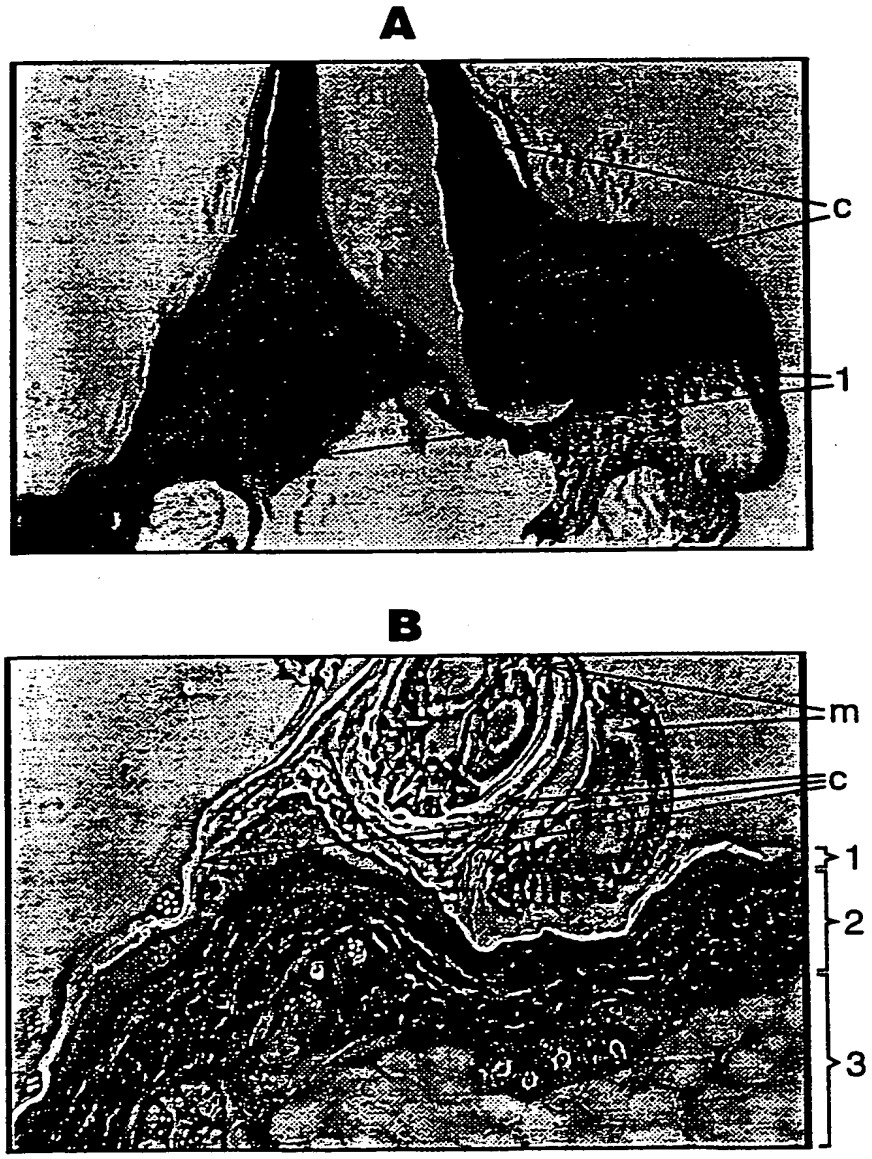
FIG. 12a HISTOLOGICAL STUDIES OF THIN HAMSTER SKIN SECTIONS STAINED WITH HAEMATOXYLIN AND EOSIN



(A) AND (B) = HISTOLOGICAL SECTIONS OF HAMSTER SKIN STAINED WITH HAEMATOXYLIN AND EOSIN; (A)=NORMAL SKIN SECTION SHOWING EPIDERMIS-1, DERMIS-2 AND SUBCUTANEOUS LAYER-3. (B)=SKIN SECTION SHOWING AN EMBEDDED TICK *(R.appendiculatus)* CEMENT CONE. STAINING: PINK= BASEMENT MEMBRANES/COLLAGEN FIBRES, UNSTAINED=RETICULIN FIBRES, BLUE=CELL NUCLEI. C REFERS TO CEMENT CONE AND M TICK MOUTH PARTS. ABOUT 20x

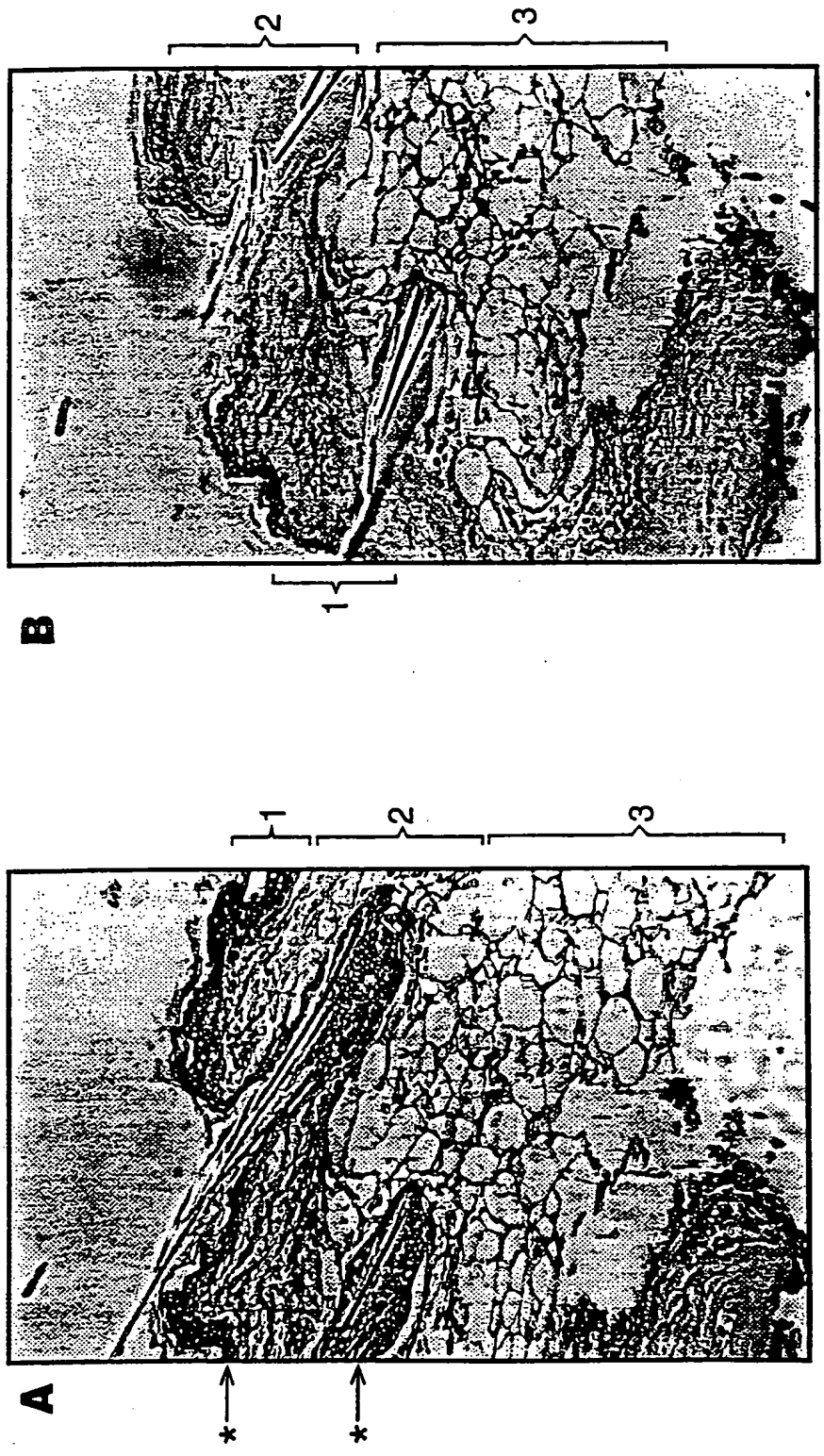
FIG. 12b

HISTOLOGICAL STUDIES OF THIN HAMSTER SKIN SECTIONS STAINED WITH HAEMATOXYLIN AND EOSIN, AND VAN GIESON STAINS.



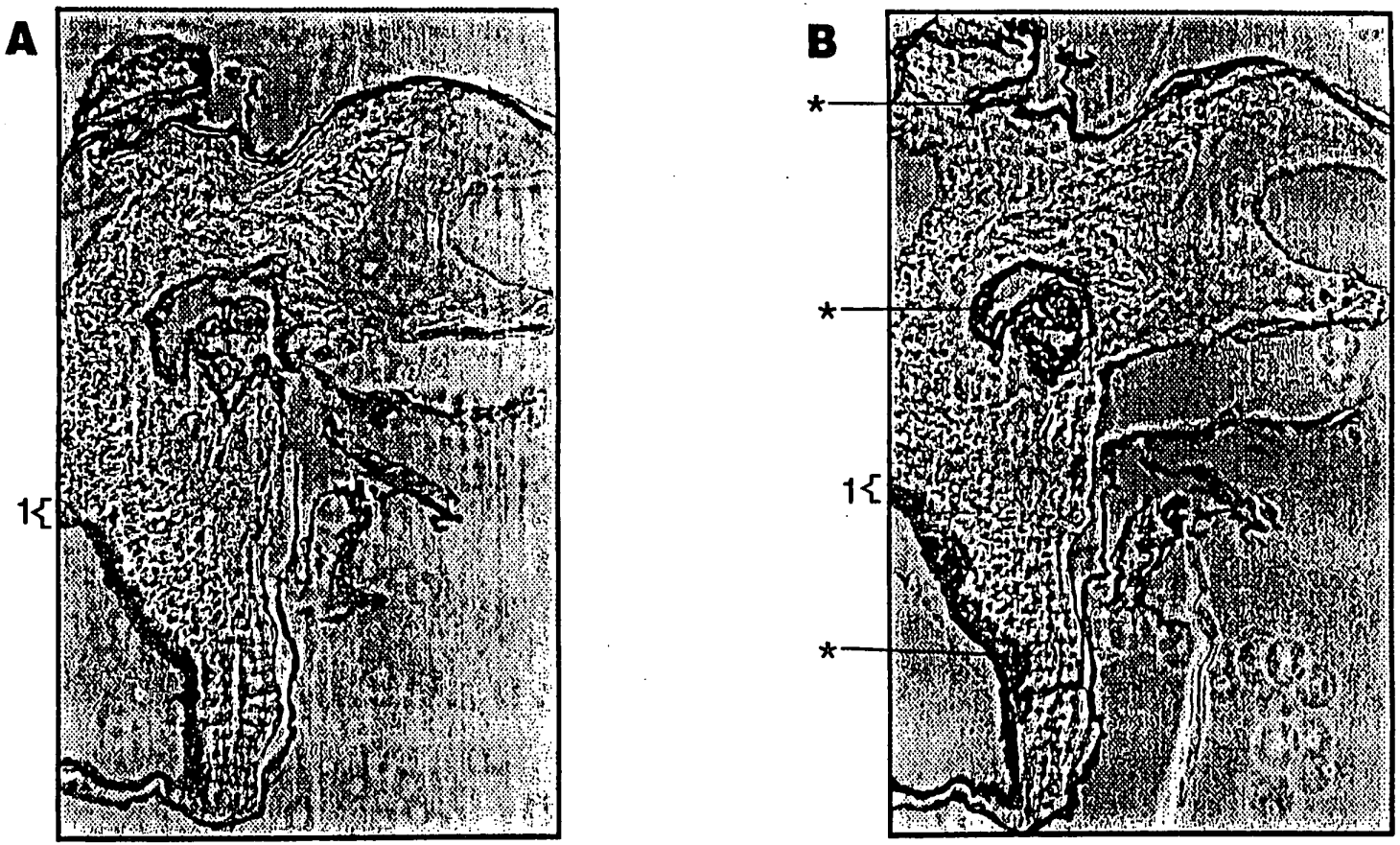
(A) AND (B) = HISTOLOGICAL SECTIONS OF HAMSTER SKIN SHOWING ATTACHED TICK *(R. appendiculatis)* CEMENT CONES (i.e. POST FEEDING) STAINED WITH (A) HAEMATOXYLIN AND EOSIN STAIN (H & E), (B) VAN GIESON STAIN. 1=EPIDERMIS, 2=DERMIS AND 3=SUBCUTANEOUS LAYER. STAINS: H & E-PINK=BASEMENT MEMBRANES/COLLAGEN FIBRES, BLUE=CELL NUCLEI, VAN GEISON-RED=COLLAGEN FIBRES, YELLOW=BASEMENT MEMBRANES/RETICULIN AND ELASTIN FIBRES. C=CEMENT CONE AND M= TICK MOUTHPARTS. ABOUT 20x.

FIG. 13a IMMUNOPEROXIDASE STUDIES ON HAMSTER SKIN SECTIONS USING ANTI-64TRP ANTISERUM



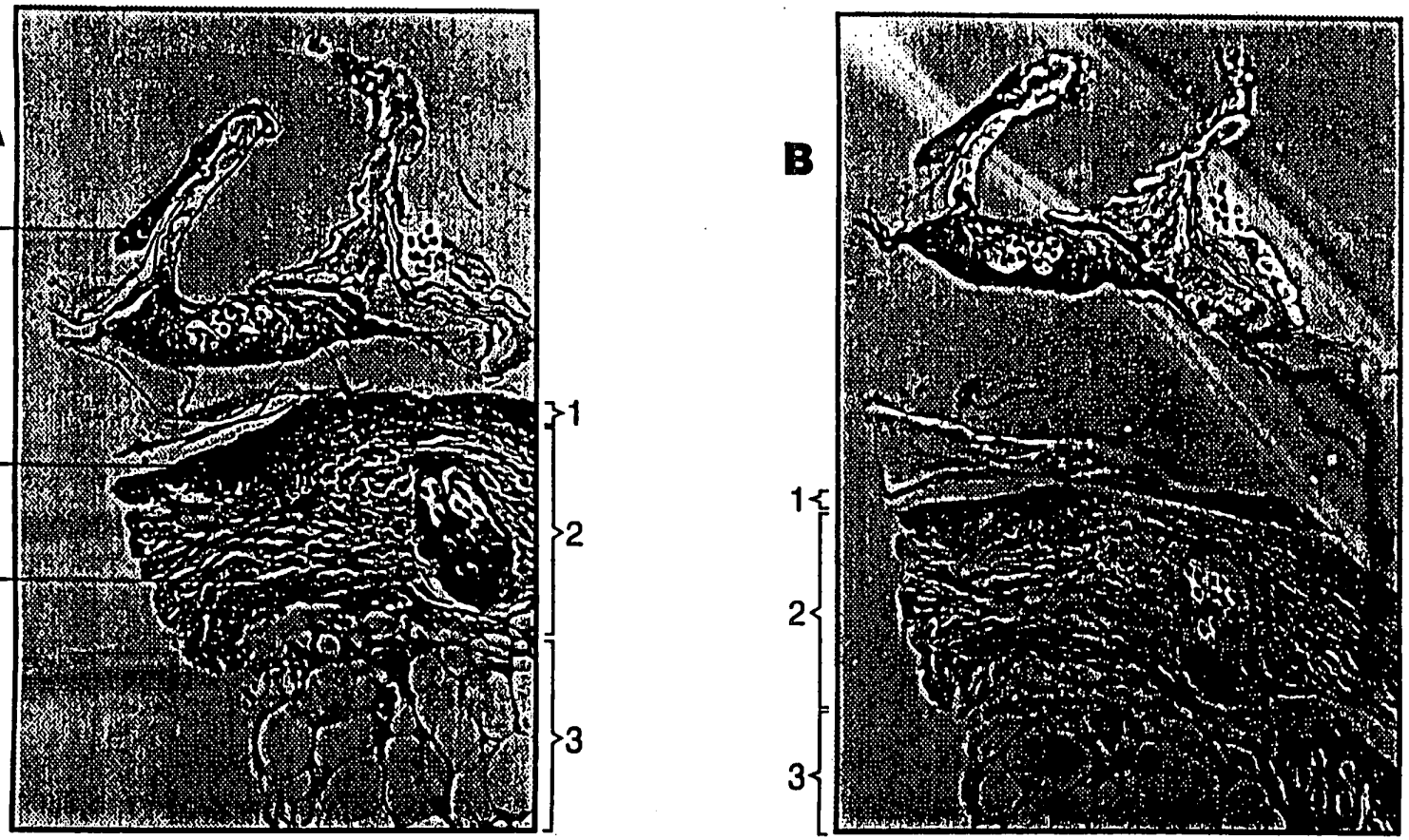
(A) AND (B) = NORMAL HISTOLOGICAL SECTIONS OF HAMSTER SKIN INCUBATED WITH ANTI-64TRP ANTISERUM AND A POSITIVE CONTROL ANTISERUM RESPECTIVELY, AND DEVELOPED WITH PEROXIDASE LINKED SECONDARY ANTISERUM. 1= EPIDERMIS, 2=DERMIS AND 3= SUBCUTANEOUS LAYER; *=AREAS OF SKIN SHOWING POSITIVE REACTIONS TO ANTI 64TRP ANTISERUM. ABOUT 20x

FIG. 13b IMMUNOPEROXIDASE STUDIES ON *R. appendiculatus* CEMENT CONE SECTIONS USING ANTI-64TRP ANTISERUM



(A) AND (B) = THIN SECTIONS OF *R. appendiculatus* CEMENT CONES INCUBATED WITH EITHER A POSITIVE CONTROL ANTI-SERUM OR ANTI-64 TRP ANTI-SERUM RESPECTIVELY, AND DEVELOPED WITH PEROXIDASE LINKED SECONDARY ANTISERUM. 1=PART OF SKIN EPIDERMIS *=AREAS OF SKIN SHOWING POSITIVE REACTIONS TO ANTI-64TRP ANTI-SERUM. ABOUT 20x

FIG. 13c IMMUNOPEROXIDASE STUDIES USING ANTI-64TRP ANTISERUM ON THIN HAMSTER SKIN SECTIONS POST FEEDING WITH *R. appendiculatus*



(A) AND (B) = THIN SECTIONS OF HAMSTER SKIN POST-FEEDING WITH *R. appendiculatus* SHOWING A CEMENT CONE STILL ATTACHED, INCUBATED WITH ANTI-64TRP ANTISERUM AND A POSITIVE CONTROL ANTISERUM RESPECTIVELY, AND DEVELOPED WITH PEROXIDASE LINKED SECONDARY ANTISERUM. 1=EPIDERMIS, 2=DERMIS AND 3=SUBCUTANEOUS LAYER. * = AREAS OF SKIN SHOWING POSITIVE REACTIONS TO ANTI 64TRP ANTISERUM. ABOUT 20x